



SEQUENCE LISTING

#3

<110> Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

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<140> 10/006,771

<141> 2001-12-10

<150> 60/250,090

<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln	
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Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg	
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His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
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Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	
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Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr	
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Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala	
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Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr	
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Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	
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Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser	
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Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
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Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

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	100	105			110	
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly						
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Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln						
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Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg						
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Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser						
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Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile						
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His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg						
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Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met						
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Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu						
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Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val						
	245		250			255
Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro						

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Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu		
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Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp		
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Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe		
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Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser		
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Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr		
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Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys		
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 Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val
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 80 85 90

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 35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala
 65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val
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<210> 5
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 <213> Homo sapiens and Mus sp.

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<220>
<221> CDS
<222> (14)..(712)
<223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light
chain V region (aa20-126), with human constant CK domain (aa127-
232) and leader (aa1-19). (pertinent to Figure 4B.)
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agc	ctg	agc	gcc	agc	gtg	ggt	gac	aga	gtg	acc	atc	acc	tgt	aag	gcc		145
Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala		
	30					35					40						
agt	cag	gat	gtg	ggt	act	tct	gta	gct	tgg	tac	cag	cag	aag	cca	ggt		193
Ser	Gln	Asp	Val	Gly	Thr	Ser	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly		
	45				50					55					60		
aag	gct	cca	aag	ctg	ctg	atc	tac	tgg	aca	tcc	acc	cgg	cac	act	ggt		241
Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Thr	Ser	Thr	Arg	His	Thr	Gly		
				65					70					75			
gtg	cca	agc	aga	ttc	agc	ggt	agc	ggt	agc	ggt	acc	gac	ttc	acc	ttc		289
Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe		
			80					85					90				
acc	atc	agc	agc	ctc	cag	cca	gag	gac	atc	gcc	acc	tac	tac	tgc	cag		337
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln		
		95					100					105					
caa	tat	agc	ctc	tat	cgg	tcg	ttc	ggc	caa	ggg	acc	aag	gtg	gaa	atc		385
Gln	Tyr	Ser	Leu	Tyr	Arg	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile		
	110					115					120						
aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat		433
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp		
					130					135					140		
gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac		481
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn		

	145	150	155	
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc				529
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu				
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caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac				577
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp				
	175	180	185	
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac				625
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr				
	190	195	200	
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc				673
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser				
	205	210	215	220
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa				712
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
	225	230		

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 <212> PRT
 <213> Homo sapiens and Mus sp.

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Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala				
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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val				
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Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys				
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Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg				
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Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys
225 230